

Search notes

110713

From: Yu, Misook
Sent: Thursday, December 18, 2003 8:45 AM
To: Schreiber, David
Subject: FW: 09873409

12-18-03, my

This is the case we discussed yesterday. Would you please align SEQ ID NOs 1-8 (proteins) against NCBI # AA073470 (812 aa protein), also align SEQ ID NOs 9-16 against NCBI # AY234788 (2906 bp cDNA). Thank you.

-----Original Message-----

From: Yu, Misook
Sent: Wednesday, December 17, 2003 11:44 AM
To: Schreiber, David
Subject: FW: 09873409

Pls let me know when you have a few minutes, I would like to discuss with you about this case. It appears that the protein sequences are deduced from two major BAC clones (about 100 kb each) and sequence search did not reveal any of the BAC clones and I wonder why.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

-----Original Message-----

From: Yu, Misook
Sent: Wednesday, December 17, 2003 9:57 AM
To: Schreiber, David
Subject: 09873409

David, Would you pls align SEQ IS NOs 1-8 (all proteins)? I would like to know how different they are. It is due this biweek. Thanks.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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Copyright (c) 1993 - 2003 Compugen Ltd.
GenCore version 5.1.6

OM nucleic - nucleic search, using sw model
Run on: December 18, 2003, 13:01:35 ; Search time 30 Seconds
3.983 Million cell updates/sec

Title: AY234788
Perfect score: 2906
Sequence: 1 ccttaattctcttaataatctc.....atgcacagtcgtgcagtga 2906

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5
Searched: 8 seqs, 20558 residues
Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 8 summaries

Database : US09873409.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	2821	97.1	2856	1 US-09-873-409-10
2	2793	96.1	3177	1 US-09-873-409-12
3	2793	96.1	3621	1 US-09-873-409-14
4	2793	96.1	3702	1 US-09-873-409-13
5	2066	71.1	2066	1 US-09-873-409-9
6	755.2	26.0	1175	1 US-09-873-409-11
7	727.2	25.0	1190	1 US-09-873-409-16
8	727.2	25.0	2021	1 US-09-873-409-15

ALIGNMENTS

RESULT 1			
US-09-873-409-10	Sequence 10, Application	US/09873409	
GENERAL INFORMATION:			
APPLICANT: Frank, Markus			
APPLICANT: Sayigh, Mohamed			
TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein			
FILE REFERENCE: 81994/268811			
CURRENT APPLICATION NUMBER: US/09/873, 409			
NUMBER OF SEQ ID NOS: 19			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 10			
LENGTH: 2856			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-873-409-10			
Query Match			

Best Local Similarity 98.3%; Pred. No. 4.4e-11; Matches 2856; Conservative 0; Mismatches 0; Indels 50; Gaps 1; Matches 2856; Conservative 0; Mismatches 0; Indels 50; Gaps 1;			
QY	1 CCTTAATTCTCTAATATCTCTCTGTGACCTTAACCATTAATATATTACATTCTT	60	Db
Db	1 CCTTAATTCTCTAATATCTCTCTGTGACCTTAACCATTAATATATTACATTCTT	60	QY
QY	121 TTAGTGAACTCATAGCAGTATGCAATTGAGCAGCTGGCTCCCTCACTTTGAAACCTTAATATATTACATTCTT	120	Db
Db	121 TTAGTGAACTCATAGCAGTATGCAATTGAGCAGCTGGCTCCCTCACTTTGAAACCTTAATATATTACATTCTT	120	QY
QY	181 CAAATAGCCGAGAGCTGCCTTCATAATTCCAGGTTATGTAAGAACCCAGTATAG	240	Db
Db	181 CAAATAGCCGAGAGCTGCCTTCATAATTCCAGGTTATGTAAGAACCCAGTATAG	240	QY
QY	241 ATAACTTCCACAGCTGGATAACCTGAATCAGTCAAGGAACTGGGATTAAA	300	Db
Db	191 ATAACTTCCACAGCTGGATAACCTGAATCAGTCAAGGAACTGGGATTAAA	300	QY
QY	301 ATGTTCTTCATTATCCATCAGACATCTCAACATTCTGAAAGGCTGATCTCA	360	Db
Db	251 ATGTTCTTCATTATCCATCAGACATCTCAACATTCTGAAAGGCTGATCTCA	360	QY
QY	361 GAAATTAGCTGGAGAGCAGTGCCTTGCTGTGCTGCTAATGCCAGTGGAGAGTACCG	420	Db
Db	311 GAAATTAGCTGGAGAGCAGTGCCTTGCTGTGCTGCTAATGCCAGTGGAGAGTACCG	420	QY
QY	421 TAGTCGAATTCTCGAGGTTATGTCGGGTTATGAGACCATATTGGAGTTGTTAGTCAG	490	Db
Db	371 TAGTCGAATTCTCGAGGTTATGTCGGGTTATGAGACCATATTGGAGTTGTTAGTCAG	490	QY
QY	481 ATGACATCGAGCTTAATGTCGGGTTATGAGACCATATTGGAGTTGTTAGTCAG	540	Db
Db	431 ATGACATCGAGCTTAATGTCGGGTTATGAGACCATATTGGAGTTGTTAGTCAG	540	QY
QY	541 AGCGCTGTTGCTGGGACCATCATGAACTACATGAACTGAGCTGGAGATGATGAGCA	600	Db
Db	491 AGCGCTGTTGCTGGGACCATCATGAACTACATGAGCTGGAGATGATGAGCA	600	QY
QY	601 CTGATGAGAGATGGAGAGCAGCAGCAGGAAATGGGATGATTATCATGGAT	660	Db
Db	551 CTGATGAGAGATGGAGAGCAGCAGCAGGAAATGGGATGATTATCATGGAT	660	QY
QY	610 TTCTTAATTATTAATGATGTTAGGGAAAGGGCTCAATGATGTTAGGGCGAA	720	Db
Db	611 TTCTTAATTATTAATGATGTTAGGGAAAGGGCTCAATGATGTTAGGGCGAA	720	QY
QY	721 AACNGAGATGCGATTCTCGGCCCTAGTCGAACCCAGATTCGTGATTAGTC	780	Db
Db	671 AACAGAGGATGCGATTCTCGGCCCTAGTCGAACCCAGATTCGTGATTAGTC	780	QY
QY	781 AGGCTACCTCTGCCCTGAGTCAGCTGCTCAAGCTGCACTGGAGAGG	840	Db
Db	731 AGGCTACCTCTGCCCTGAGTCAGCTGCTCAAGCTGCACTGGAGAGG	840	QY
QY	841 CGACGAAAGTCGCACTACATCGGGAGCACCGCTTCTACTATTCGAGTGTG	900	Db
Db	791 CGACGAAAGTCGCACTACATCGGGAGCACCGCTTCTACTATTCGAGTGTG	900	QY
QY	901 ATTGATGTTGACCTAAAGGATGGAATGCTGGGGAGAACAGGAGCATGCTGA	960	Db
Db	851 ATTGATGTTGACCTAAAGGATGGAATGCTGGGGAGAACAGGAGCATGCTGA	960	QY
QY	961 TGGCAACAGGAGCTATATTACACTGTCAGGATTAAGAGCTGTG	1020	Db
Db	911 TGGCAACAGGAGCTATATTACACTGTCAGGATTAAGAGCTGTG	1020	QY
QY	1021 AACGAGATGCGATTCTCGGCCCTAGTCGAACCCAGATTCGTGATTAGTC	1080	Db

Db	971	AACAGATGGAGTCATGACATATTCTACTGAGAAGAACCAACTCACTCTGACT	1030	QY	2161	CATGTGAGGGATTAGAGTTGAGAGTCCTTCTCTATCCATGCCAGATG	2220
QY	1081	CTCTGAAGAGCATCAGTCAGTCAGCTCATTCAGGCTTCAAGGAACTCTAAAG	1140	Db	2111	CATGTGAGGGATTAGAGTCCTTCTCTATCCATGCCAGATG	2170
Db	1031	CTGTGAAGAGCATCAGTCAGCTCATTCAGGCTTCAAGGAACTCTAAAG	1090	QY	2221	TTTCATCTCTCGTGCTATCCCTCATGATGAGCTCTTCTCTATCCATGCCAGATG	2280
QY	1141	AGATAGTCGTTCTCGAGTCAGCTCATTCAGGCTTCAAGGAACTCTAAAG	1200	Db	2171	TTTCATCTCTCGTGCTATCCCTCATGATGAGCTCTTCTCTATCCATGCCAGATG	2230
Db	1091	AGATAGTCGTTCTCGAGTCAGCTCATTCAGGCTTCAAGGAACTCTAAAG	1150	QY	2221	GGGAGGGCTTGGAGAACACTCTGTCACCTCTCAGAGACTTTATGACCCG	2340
QY	1201	CTTTGTGGCTCTGGAGCATGCTCTGTCATAATGAGCTGTATCCAGTATT	1260	Db	2231	GGAGCAGGGCTTGGAGAACACTCTGTCACCTCTCAGAGACTTTATGACCCG	2290
Db	1151	CTTTGTGGCTCTGGAGCATGCTCTGTCATAATGAGCTGTATCCAGTATT	1210	QY	2341	TGAAAGGAAGTGTGTTGATGGATGCAAAGAATGAGTGTGAGCTTGTGAGA	2400
QY	1261	CATCATCATCTTCGAAAAATTAAACCATTTGAAATATGAAACCACTAAAGC	1320	Db	2231	TGAAAGGAAGTGTGTTGATGGATGCAAAGAATGAGTGTGAGCTTGTGAGA	2350
Db	1211	CATCATCATCTTCGAAAAATTAAACCATTTGAAATATGAAACCACTAAAGC	1270	QY	2401	GTTCCTAAATGCACTGTTCTCAAGAGCCTGCTTCAACTCAGCTTGTGAGA	2460
QY	1321	ATGAAGAGAAATTATTCGATATTCGATTTGGGTTATTGCTTGTGCTATT	1380	Db	2351	GTTCCTAAATGCACTGTTCTCAAGAGCCTGCTTCAACTCAGCTTGTGAGA	2410
Db	1271	ATGATGAGAAATTATTCGATATTCGATTTGGGTTATTGCTTGTGCTATT	1330	QY	2461	ACATGGCTTATGGCAACGCGCTGTCGCAACTTGTGAGACTTGTGAGA	2520
QY	1381	ATTTCATGGAGGGATTATTCACCGAGGCGAGGGAAATTAAACGTTGAGAATG	1440	Db	2411	ACATGGCTTATGGCAACGCGCTGTCGCAACTTGTGAGACTTGTGAGA	2470
Db	1331	ATTTCATGGAGGGATTATTCACCGAGGCGAGGGAAATTAAACGTTGAGAATG	1390	QY	2521	ATCCAGCAATATCCATCTTATGAGGCTCCCTGAGAAATCACACACAGTG	2580
QY	1441	ACTGGCCCTCAAAAGCATGTATATCAGGATATTGCGCTGGTTGATGAAAGGAAACA	1500	Db	2471	ATCAGCAATATCCATCTTATGAGGCTCCCTGAGAAATCACACACAGTG	2530
Db	1391	ACTGGCCCTCAAAAGCATGTATATCAGGATATTGCGCTGGTTGATGAAAGGAAACA	1450	QY	2581	GACTGAAGGGAGCACACGCTTCTGGCGCCAGAAACAAAGACTAGCTATGCAAGGGCTC	2640
QY	1501	GCACAGGGGCTTCACACAAATTAGCGATAGATAGCACAAATTCAAGGAGCAAC	1560	Db	2531	GACTGAAGGGAGCACACGCTTCTGGCGCCAGAAACAAAGACTAGCTATGCAAGGGCTC	2590
Db	1451	GCACAGGGGCTTCACACAAATTAGCGATAGATAGCACAAATTCAAGGAGCAAC	1510	QY	2641	TTCTCCAAACCAAAATTATGGTGGATGAGCTTGTGAGCTTGTGAGAATGAGA	2700
QY	1561	GTTCAGGGATTGGCTTAAACACAAATTGCAACTACATGGACTTCAGTATCATT	1620	Db	2591	TTCTCCAAACCAAAATTATGGTGGATGAGCTTGTGAGAATGAGA	2650
Db	1511	GTTCAGGGATTGGCTTAAACACAAATTGCAACTACATGGACTTCAGTATCATT	1570	QY	2701	GTGAGAAGGGTTTCAAGGATGCGCTTGTGAGAAAGCCAGGCGGAGGACATGCCAGTG	2760
QY	1621	CTTTATATATGGGAGATGACATCTCTGATGAGTATGCTCCAGACTTGCCTG	1680	Db	2651	GTGAGAAGGGTTTCAAGGATGCGCTTGTGAGAAAGCCAGGCGGAGGACATGCCAGTG	2710
Db	1571	CTTTATATATGGGAGATGCGACTTCTGATCTGAGTATGCTCCAGACTTGCCTG	1630	QY	2761	TCACTCACGGCTCTGCAATTCTGAGAGCAGATGTTGATGTCGACAAATGGAA	2820
QY	1681	TGACAGGATGATGAGTGAACCGCAGCAACTGAGCTTGGAGATATGACTATAGTCAT	1740	Db	2711	TCACTCACGGCTCTGCAATTCTGAGAGCAGATGTTGATGTCGACAAATGGAA	2770
Db	1631	TGACAGGATGATGAGTGAACCGCAGCAACTGAGCTTGGAGATATGACTATAGTCAT	1690	QY	2821	AGATAAGGAAAGAGAAACTCATGAGAGCTCTGAGAAATGAGCAATATTTAAGT	2880
QY	1741	TTAGCATCTGGAGAGTAGCAACTGAGCTTGGAGATATGACTATAGTCAT	1800	Db	2771	AGATAAGGAAAGAGAACTCATGAGAGCTCTGAGAAATGAGCAATATTTAAGT	2830
Db	1691	TTAGCATCTGGAGAGTAGCAACTGAGCTTGGAGATATGACTATAGTCAT	1750	QY	2881	TAGTGAATGCACTGAGCTTGGAGA	2906
QY	1801	TAACAGGGAAAGACCTTCGAGAAATGAGAGATGCTCAGACTCACACGAA	1860	Db	2831	TAGTGAATGCACTGAGCTTGGAGA	2856
Db	1751	TAACAGGGAAAGACCTTCGAGAAATGAGAGATGCTCAGACTCACACGAA	1810				
QY	1861	ATACCTCGAGAAAGACAGATATTGGAGCTTGTGAGTCAGCTCATGCTTTAT	1920				
Db	1811	ATACCTCGAGAAAGACAGATATTGGAGCTTGTGAGTCAGCTCATGCTTTAT	1870				
QY	1921	ATTTTGCCATAGTCAGCAGGGTTTGATGAGCTTGTGAGTCAGCTCATGCTAA	1980				
Db	1871	ATTTTGCCATAGTCAGCAGGGTTTGATGAGCTTGTGAGTCAGCTCATGCTAA	1930				
QY	1981	CCCCAGAGGGCTTCATAGTTTACTGCAATGCACTTGTGAGTCAGCTCATGCTAA	2040				
Db	1931	CCCCAGAGGGCTTCATAGTTTACTGCAATGCACTTGTGAGTCAGCTCATGCTAA	1990				
QY	2041	AACAGCTCTTGTGAGTCAGCTCATGCTTTACTGCAATGCACTTGTGAGTCAGCTCATGCTAA	2100				
Db	1991	AACAGCTCTTGTGAGTCAGCTCATGCTTTACTGCAATGCACTTGTGAGTCAGCTCATGCTAA	2050				
QY	2101	CCTGTTGAAAGAACCAAAATAGACAGCCGCACTAACAGGGAAAGCCAGACA	2160				
Db	2051	CCTGTTGAAAGAACCAAAATAGACAGCCGCACTAACAGGGAAAGCCAGACA	2110				

RESULT 2

USS-09-873-409-12

; Sequence 12, Application US/09873409

; GENERAL INFORMATION:

; APPLICANT: Frank, Markus

; APPLICANT: Sayegh, Mohamed

; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof

; FILE REFERENCE: 8194/268611

; CURRENT APPLICATION NUMBER: US/09/873,409

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 12

; LENGTH: 3177

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: Note

LOCATION: (198)..(198)
 OTHER INFORMATION: n at position 198 represents any nucleotide (A, T, C or G)
 US-09-871-409-12

Query Match 96.1%; Score 2793; DB 1; Length 3177;
 Best Local Similarity 100.0%; Pred. No. 5.2a-11; Mismatches 0; Indels 0; Gaps 0;
 Matches 2793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTTTCTTCTTGTGATTCATAGCAGTTATGCTGAGTCAGTGGCCCTACTTGAA 173
 Db 385 GTTCTCTTGTGATTCATAGCAGTTATGCTGAGTCAGTGGCCCTACTTGAA 444

QY 174 ACCTTGCAATAGCCGAGGAGCTGCTTCAATTTCAGGTTATGCTGAGTCAGTGGAA 233
 Db 445 ACCTTGCAATAGCCGAGGAGCTGCTTCAATTTCAGGTTATGCTGAGTCAGTGGAA 504

QY 234 AGTATAGATACCTTCCAGCTGATAAACCTGAATTCATAGAAGGACTGTGAA 293
 Db 505 AGTATAGATACCTTCCAGCTGATAAACCTGAATTCATAGAAGGACTGTGAA 564

QY 294 TTAAAAATGTTCTTCATAATTCCATAGACCATCTATCAAGTCTGCTCAATGCACTGGAG 353
 Db 565 TTAAAAATGTTCTTCATAATTCCATAGACCATCTATCAAGTCTGCTCAATGCACTGGAG 624

QY 354 ATATTCAGAAATTAAGTCTGGAGAGACGTCGCTTGTGCTCAATGCACTGGAG 413
 Db 625 ATATTCAGAAATTAAGTCTGGAGAGACGTCGCTTGTGCTCAATGCACTGGAG 684

QY 414 AGTACGGTAGTCCAGCTTCTCGAGGTTATGATCCGGAGTAGCTTATCATGGG 473
 Db 685 AGTACGGTAGTCCAGCTTCTCGAGGTTATGATCCGGAGTAGCTTATCATGGG 744

QY 474 GATGAGATGACATAGAGCTTAATGTCGGCATATGGAGGCTTATGGAGTGGT 533
 Db 745 GATGAGATGACATAGAGCTTAAATGTCGGCATATGGAGGCTTATGGAGTGGT 804

QY 534 AGTCAGAGGCTGTTGTCGGGACCATCTAGTACAACTAACGATGGAGGAGAT 593
 Db 805 AGTCAGAGGCTGTTGTCGGGACCATCTAGTACAACTAACGATGGAGGAGAT 864

QY 594 GATGAGACTGAG 653
 Db 865 GATGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 924

QY 654 ATGGAGTTCTTAATTAATTTATACATGGTAGGAAALAGGAGGCTAAATGAGTGG 713
 Db 925 ATGGAGTTCTTAATTAATTTATACATGGTAGGAAALAGGAGGCTAAATGAGTGG 984

QY 714 GGGCGAAACGGAGATCGGATATGCTCGGCCCTAGTGGAAACCCAGATTGATT 773
 Db 985 GGGCGAAACGGAGGATCGGAACTGGCTTAGTGGAAACCCAGATTGATT 1044

QY 774 TTAGTGAGGTACGTCTGCCCTGGATTAGAAGGAAGGAGTCAGTGTCACTG 833
 Db 1045 TTAGTGAGGTACGTCTGCCCTGGATTAGAAGGAAGGAGTCAGTGTCACTG 1104

QY 834 GAGAGGGCGACCAAGGTCGCACTACATGCTGGTAGCACCGACTTCTACTATCGA 893
 Db 1105 GAGAGGGCGACCAAGGTCGCACTACATGCTGGTAGCACCGACTTCTACTATCGA 1164

QY 894 AGTGCAGATTGATGTTGACCTAAAGGATGGAATCTGGGAGGAGGACATGCT 953
 Db 1165 AGTGCAGATTGATGTTGACCTAAAGGATGGAATCTGGGAGGAGGACATGCT 1224

QY 954 GAACTATGGCAACGGGCTTATTTACTGTGATGTCACAGGATTAATAAA 1013
 Db 1225 GAACTATGGCAACGGGCTTATTTACTGTGATGTCACAGGATTAATAAA 1284

QY 1014 GCTGATGACGATGATGAGTCATGACATATTCTACTGAAGAAGGACCAACTACTCT 1073
 Db 1285 OCTGATGACAGATGGATGTCATGACATATTCTACTGAAGAAGGACCAACTCT 1344

QY 1074 CTGCACTCTGAGAGACATCAAGTCAGACTTCATGACAAAGGCTGAGGAATCCACCAA 1133

Db 1345 CTGCACTCTGAGAGACATCAAGTCAGACTTCATGACAAAGGCTGAGGAATCCACCAA 1404
 QY 1134 TCTAAAGAGATAAGTCTCTCTGAGTCAGTGGCCCTACTTGAA 1193
 Db 1405 TCTAAAGAGATAAGTCTCTCTGAGTCAGTGGCCCTACTTGAA 1464

QY 1194 GAACTGCCCTTGTGTTCTGGGACAATGGCTCTGCTCAATGGACTGTCA 1253
 Db 1465 GAATGCCCTTGTGTTCTGGGACAATGGCTCTGCTCAATGGACTGTCA 1524

QY 1254 GATTTTCCATCATCTTCTGCAAAATTATACCTGTGTTGAAATAATGATAAAACCA 1313
 Db 1525 GATTTTCCATCATCTTCTGCAAAATTATACCTGTGTTGAAATAATGATAAAACCA 1584

QY 1314 TTAAAGCTGAGAGAAATTATCCCTGATATTCGCTATGGCTTGTGTT 1373
 Db 1585 TTAAAGCTGAGAGAAATTATCCCTGATATTCGCTATGGCTTGTGTT 1644

QY 1374 GTCAGTTTCTGCAAGGATTTACGGAGAGAGGGAAATTACATGAGA 1433
 Db 1645 GTCAGTTTCTGCAAGGATTTACGGAGAGGGAAATTACATGAGA 1704

QY 1434 TTAAAGCTGAGAGAAATTATCCCTGATATTCGCTATGGCTTGTGTT 1493
 Db 1705 TTAAAGCTGAGAGAAATTATCCCTGATATTCGCTATGGCTTGTGAAAG 1764

QY 1494 GAAACAGACAGAGGGCTGACACAACTATGGCTATTCGCAAGATAGC 1553
 Db 1765 GAAACAGACAGAGGGCTGACACAACTATGGCTATTCGCAAGATAGC 1824

QY 1554 GCAACAGGTTCCAGGATGGCTCTACACAAATGCAACTAACATGGACTTCAGT 1613
 Db 1825 GCAACAGGTTCCAGGATGGCTCTACACAAATGCAACTAACATGGACTTCAGT 1884

QY 1614 ATCATTTCTTATATGATGGAGGATGATGTTATGGAGGATATGGCTGTTGATGAAAG 1673
 Db 1885 ATCATTTCTTATATGATGGAGGATGATGTTATGGAGGATATGGCTGTTGATGAAAG 1944

QY 1674 CTTCGCGTACAGGAGATGATGAAACCGAGCAATGAGCTTCTCATTCTGAGATGCTCCAACTA 1733
 Db 1945 CTTCGCGTACAGGAGATGATGAAACCGAGCAATGAGCTTCTCATTCTGAGATGCTCCAACTA 2004

QY 1734 CAAGACTTACAGTGTGAAAGATGAGCTGAGCTGAGCTTGGAGAAATACTGACTTA 1793
 Db 2005 CAAGACTTACAGTGTGAAAGATGAGCTGAGCTTGGAGAAATACTGACTTA 2064

QY 1794 GTGTCATTACAAAGGAAAGAGCTTCCGAGCAATGAGCTGAGATGCTCAGCTAA 1853
 Db 2065 GTGTCATTACAAAGGAAAGAGCTTCCGAGCAATGAGCTGAGATGCTCAGCTAA 2124

QY 1854 CACGAAATACCTGAAAGGACAGATAATGGAGGCTGATGTCAGCTGAC 1913
 Db 2125 CACGAAATACCTGAAAGGACAGATAATGGAGGCTGATGTCAGCTGAC 2184

QY 1914 TTATATTCTGCTATGAGCAGGGTTGATGTCAGTGGCCCTATTAACTCAAGCTGA 1973
 Db 2185 TTATATTCTGCTATGAGCAGGGTTGATGTCAGTGGCCCTATTAACTCAAGCTGA 2244

QY 1974 CGAATGACCCAGAGGGCTGTCAGTGGCTGATGTCAGTGGCCCTATTAACTCAAGCTGA 2033
 Db 2245 CGAATGACCCAGAGGGCTGTCAGTGGCTGATGTCAGTGGCCCTATTAACTCAAGCTGA 2304

QY 2034 ATCGAAAAAGCTGCTGTCAGTGGCTGATGTCAGTGGCCCTATTAACTCAAGCTGA 2023

QY 2305 ATCGAAAAAGCTGCTGTCAGTGGCTGATGTCAGTGGCCCTATTAACTCAAGCTGA 2364

QY 2094 CTGTTGCTCTGTGAGAAGAACAAATAGACAGCGCAGTCAGAGGAAAG 2153
 Db 2365 CTGTTGCTCTGTGAGAAGAACAAATAGACAGCGCAGTCAGAGGAAAG 2424

QY 2154 CGAACACATGAGAGGAGATTAGGTTGAGAGACTCTGCTGAGGAAATCCACCAA 2213

Db 2425 CAGACACATGAGGAAATTAGAGTTCTGAGAAGCTCTTCTTATCATGPGC 2484
 Qy 2214 CTCAGATGTTTCACTCTCGTGCCTAATCCCTCACTGATGACGGAGAACAGTAGCA 2273
 Db 2485 CTCAGATGTTTCACTCTCGTGCCTAATCCCTCACTGATGACGGAGAACAGTAGCA 2544
 Qy 2274 TTCTGCGAGGAGCGGGCTGTTGAAAGACACTCTGTCAGTTGAGCGAGAACAGTAGCA 2333
 Db 2545 TTCTGCGAGGAGCGGGCTGTTGAAAGACACTCTGTCAGTTGAGCGAGAACAGTAGCA 2604
 Qy 2334 GACCCCGTCAAGAGAACAGTGTGTTGATGTCGTTGAGGATGCAAGAATGATGACAG 2393
 Db 2605 GACCCCGTCAAGAGAACAGTGTGTTGATGTCGTTGAGGATGCAAGAATGATGACAG 2664
 Qy 2394 TGGTCCTCGTCCCAATATGCAATGCTTCAGAGAGCTGCTCTCACTCGCAGATT 2453
 Db 2665 TGGTCCTCGTCCCAATATGCAATGCTTCAGAGAGCTGCTCTCACTCGCAGATT 2724
 Qy 2454 GCTGAGAACATCGCCTATGGTACAGACAGCCGGTGGGCCATTAGTGGAGTCAGAA 2513
 Db 2725 GCTGAGAACATCGCCTATGGTACAGACAGCCGGTGGGCCATTAGTGGAGTCAGAA 2784
 Qy 2514 GCCCCAATGAGAACATTCATCTTTATGAGGCTCCCTGAGAAATACACCA 2573
 Db 2785 GGGCAATGAGAACATTCATCTTTATGAGGCTCCCTGAGAAATACACCA 2844
 Qy 2574 CAAAGTGGACTGAAAGGAGCACAGCTTCTGGGGCGAGAACAAAGACTGACTATGCA 2633
 Db 2845 CAAAGTGGACTGAAAGGAGCACAGCTTCTGGGGCGAGAACAAAGACTGACTATGCA 2904
 Qy 2634 AGGGCTCTCTCCRAAAACCCAAATTATGGTGGAGACGACTTCACCCCTGAT 2693
 Db 2905 AGGGCTCTCTCCRAAAACCCAAATTATGGTGGAGACGACTTCACCCCTGAT 2964
 Qy 2694 ATGACAGTGGAGGGTTCAGATGCCCTGATAAAGCCAGGACGGAGACATGC 2753
 Db 2965 ATGACAGTGGAGGGTTCAGATGCCCTGATAAAGCCAGGACGGAGACATGC 3024
 Qy 2754 CTAGTGGTCACTCACAGGCTCTGCAATTAGGAGGAGATTGATGTTCTGAC 2813
 Db 3025 CTAGTGGTCACTCACAGGCTCTGCAATTAGGAGGAGATTGATGTTCTGAC 3084
 Qy 2814 ATGGAAAGATAAAGGACAGGGACTCATCAAGAGCTCTGAAATGAGCATAT 2873
 Db 3085 ATGGAAAGATAAAGGACAGGGACTCATCAAGAGCTCTGAAATGAGCATAT 3144
 Qy 2874 TTAGTGTAGTGTGACAGTGTGAGTGA 2906
 Db 3145 TTTAAGTGTAGTGTGACAGTGTGAGTGA 3177

RESULT 3

US-09-873-409-14

; Sequence 14, Application US/03873409

; GENERAL INFORMATION:

; APPLICANT: Frank, Markus

; TITLE OF INVENTION: A Gene Encoding a Multi-drug Resistance Human P-Glycoprotein

; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof

; FILE REFERENCE: B1/94/28611

; CURRENT APPLICATION NUMBER: US/09/873, 409

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 14

; LENGTH: 3621

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-873-409-14

Query Match 95.1%; Score 2793; DB 1; Length 3621;
 Best Local Similarity 100.0%; Prcd. No. 4 6e-11; Mismatches 0; Indels 0; Gaps 0;

Matches 2793; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1194 GAATGGCCTTTCGGTTCGGGACATGGCTCTGTCATAAAGAACCTGTCATCCA 1253
 Db 1909 GAATGGCCTTTCGGTTCGGGACATGGCTCTGTCATAAAGAACCTGTCATCCA 1968
 QY 1254 GATTTCCATCATCTTGCAGAAATTATACCATGTTGGAAATAATGATAAACCA 1313
 Db 1969 GATTTCCATCATCTTGCAGAAATTATACCATGTTGGAAATAATGATAAACCA 2028
 QY 1314 TAAGCATCATGAGAAATTATTCAGTATATGCTATTGTTGGGTTATTGCTT 1373
 Db 2029 TAAGCATCATGAGAAATTATTCAGTATATGCTATTGTTGGGTTATTGCTT 2088
 QY 1374 GTCACTTTCAGGGATTTCAGGTTACGAGGAAATTACCACTGTTGGAAATAATGATAAACCA 2143
 Db 2089 GTCACTTTCAGGGATTTCAGGTTACGAGGAAATTACCACTGTTGGGTTATTGCTT 2148
 QY 1434 TAAGACACTTGCCCTAAGCCATGTTATCAGGATTATGCTGGTTGATGAGAAG 1493
 Db 2149 TAAGACACTTGCCCTAAGCCATGTTATCAGGATTATGCTGGTTGATGAGAAG 2208
 QY 1494 GAACACGACAGGAGGCTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 2269
 Db 2209 GAACACGACAGGAGGCTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 2268
 QY 1554 GCAACAGGTTCAAGGCTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 2288
 Db 2269 GCAACAGGTTCAAGGCTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 2328
 QY 1614 ATCATTCCTTATATGATGGGAGATGACATTCCTGATTGCTGAGTTGCTCCAGTA 1673
 Db 2329 ATCATTCCTTATATGATGGGAGATGACATTCCTGATTGCTGAGTTGCTCCAGTA 2389
 QY 1674 CTTGGCTGACAGGATGATGTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 1733
 Db 2389 CTTGGCTGACAGGATGATGTTGACACAAATTACCATGAGATATTCAGCAGAGGAAATTACCATGAGA 2448
 QY 1734 CAAGACACTTAACTGCTGAAAGTAGCAGCTGAGCTTGGAAATAATGAGCTATA 1793
 Db 2449 CAAGACACTTAACTGCTGAAAGTAGCAGCTGAGCTTGGAAATAATGAGCTATA 2508
 QY 1794 GTGTCATTAACAGGAAAGGCCTCGAGCAAATGATGAGATGCTTCAACTCAA 1853
 Db 2509 GTGTCATTAACAGGAAAGGCCTCGAGCAAATGATGAGATGCTTCAACTCAA 2568
 QY 1854 CACAGAAATACCTCGAGAAAGCACAGATTATGAGCTGTTATGACTTCACTGCC 1913
 Db 2569 CACAGAAATACCTCGAGAAAGCACAGATTATGAGCTGTTATGACTTCACTGCC 2628
 QY 1914 TTATATTTGCTATCGAGAGGGTTGAGTTGGCCTTAAATCACTGGA 1973
 Db 2629 TTATATTTGCTATCGAGAGGGTTGAGTTGGCCTTAAATCACTGGA 2688
 QY 1974 CGAATGACCCAGAGGGCATGTTCACTAGTTTACTGCAATTGAGCTATGCC 2033
 Db 2689 CGAATGACCCAGAGGGCATGTTCACTAGTTTACTGCAATTGAGCTATGCC 2748
 QY 2034 ATCGGAAAAAGCTGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2093
 Db 2749 ATCGGAAAAAGCTGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2808
 QY 2094 CTGTTGCTTGTGAGGGAAATTAGAGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2153
 Db 2809 CTGTTGCTTGTGAGGGAAATTAGAGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2868
 QY 2154 CGAGCACATGTGAGGGAAATTAGAGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2213
 Db 2869 CGAGCACATGTGAGGGAAATTAGAGTTGAGAAAGAACCAAATAGACAGCCACTGAGAAAG 2928
 QY 2214 CGAGATTTCTATCCCGGTATCCCTCGAGTATGAGCAGGAAAGACAGTAGCA 2273
 Db 2929 CGAGATTTCTATCCCGGTATCCCTCGAGTATGAGCAGGAAAGACAGTAGCA 2988
 QY 2274 TTGGGGAGCAAGGGCTGGGAAAGACACTCTGTTCACTCTGAGACTT 2333

RESULT 4
 US-09-873-409-13
 Sequence 13, Application US/09873409
 GENERAL INFORMATION:
 APPLICANT: Frank, Markus
 APPLICANT: Sayegh, Mohamed
 TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
 TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
 FILE REFERENCE: 819594/248611
 CURRENT APPLICATION NUMBER: US/09/873, 409
 CURRENT FILING DATE: 2001-06-05
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 13
 LENGTH: 3702
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Note
 LOCATION: (723) OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)
 US-09-873-409-13

Query Match: 96.1%; Score: 2793; DB: 1; Length: 3702;
 Best Local Similarity: 100.0%; Pred. No.: 4_5e-11;
 Matches: 2793; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)

QY 114 GTRTCTTAGTGTAACTCATAGCACTGTTGGCATGGAGCACTGCTTCACTCTGAGACTT 173

QY	174	ACCTTCGCAATASGCCGAGGAGCTCCCTCATATTCCAGGTTATGCAAGAACCC	233	QY	1254	GTATTTCATCATTTGCAAAATTATAACCGTGTGGAATATGCAAAACCA	1313
Db	970	ACCTTCGCAATAGCCCGAGGAGCTCCCTCATATTCCAGGTTATGCAAGAACCC	1029	Db	2050	GTATTTCATCATTTGCAAAATTATAACCGTGTGGAATATGCAAAACCA	2109
QY	234	AGTATAGATACTTTCACAGCTGAGATAAACCTGAACTCATAGAAGGAACTGTGGA	293	QY	1314	TAAGCATGAGAAMATTATTCATGATAATCGTCATTGGGTATTGCTT	1373
Db	1030	AGTATAGATACTTTCACAGCTGAGATAAACCTGAACTCATAGAAGGAACTGTGGA	1089	Db	2110	TAAGCATGAGAAMATTATTCATGATAATCGTCATTGGGTATTGCTT	2169
QY	294	TTTAAAAATGTTCTTCATATTACATAGAACCTATCAAGAACCTATCAAGATCTGAA	353	QY	1374	TCAGTATTTCATGAGGATTATTCAGGAGGAGGGAAATTAAAGATGAGA	4433
Db	1090	TTTAAAAATGTTCTTCATATTACATAGAACCTATCAAGAACCTATCAAGATCTGAA	1089	Db	2170	GTCACTTATTCATGAGGATTATTCAGGAGGAGGGAAATTAAAGATGAGA	2229
QY	354	AATCTCAGAAATTAACTGAGACAGCTGCGCTGGTCAATGCCAGTGGGAG	413	QY	1434	TAAGACATTGSCCTTCAGCAGTATTCAGGATATCGCTGGTTGATGAAAG	1493
Db	1150	AATCTCAGAAATTAACTGAGACAGCTGCGCTGGTCAATGCCAGTGGGAG	1209	Db	2230	TAAGACATTGSCCTTCAGCAGTATTCAGGATATCGCTGGTTGATGAAAG	2289
QY	414	AGTACGGTAGCCAGCTCTGAGAGGTTATGACCCGATGAGCTTATGAGGTC	473	QY	1494	GAACAGCAGAGGGCTGACACAAATTAGCCATAGATAAGCAGAACATTCAAGGA	1553
Db	1210	AGTACGGTAGCCAGCTCTGAGAGGTTATGACCCGATGAGCTTATGAGGTC	1269	QY	1554	GAACAGGTTCCAGGATTGCGCTTAACACAAATGAGGAGGAAATGCTTACATGGG	2149
QY	474	GATGAGAATGACATAGACGTTAAATGTCGGCATATTGAGAACCATATGGAGT	533	Db	2290	GAACACGACAGAGGGCTGACACAAATTAGCCATAGATAAGCAGAACATTCAAGGA	2290
Db	1270	GATGAGAATGACATAGACGTTAAATGTCGGCATATTGAGAACCATATGGAGT	1329	Db	2350	GAACAGGTTCCAGGATTGCGCTTAACACAAATGAGGAGGAAATGCTTACATGGG	2409
QY	534	AGTCAGAGCCGTTTGTGCGACCCATCGAGAACATTCAGATGGAGAT	593	QY	1614	ATCATTCTTATATGGATGGAGTGCATTCGATCTGAGATTGCTCCAGTA	1673
Db	1330	AGTCAGAGCCGTTTGTGCGACCCATCGAGAACATTCAGATGGAGAT	1389	Db	2410	ATCATTCTTATATGGATGGAGTGCATTCGATCTGAGATTGCTTCCAGTA	2469
QY	534	GATGACTGATGAGAGATGGAGAGGAGGAGGAGAACGAAATGCTTACATGGT	653	QY	1674	CTTCGGTCAAGGATGATTGAAACCCAGGAAATGAGTGGATTGCGAACAAAGATAG	1733
Db	1390	GATGACTGATGAGAGATGGAGAGGAGGAGAACGAAATGCTTACATGGT	1449	Db	2470	CTTCGGTCAAGGATGATTGAAACCCAGGAAATGAGTGGATTGCGAACAAAGATAG	2529
QY	654	ATGGAGTTCTAAATTAAATACATTTGAGGGAAAAGGAGCTCAATGAGGA	713	QY	1734	CAAGACTTAAGCATGCTGAGAAGATGAGCTGAACTGAGCTTGGAGATACTACTATA	1793
Db	1450	ATGGAGTTCTAAATTAAATACATTTGAGGGAAAAGGAGCTCAATGAGGA	1509	Db	2530	CAAGACTTAAGCATGCTGAGAAGATGAGCTGAACTGAGCTTGGAGATACTACTATA	2589
QY	714	GCGCAGAACAGAGGATGCCAATGCTGCGCTAGTCGAACCCAGATTCGATT	773	QY	1794	GTGTCATTAACAGGAAACGCTTCAGCAATGATGAGAGAGCTTCAGCTCA	1853
Db	1510	GCGCAGAACAGAGGATGCCAATGCTGCGCTAGTCGAACCCAGATTCGATT	1569	Db	2590	GTGTCATTAACAGGAAACGCTTCAGCAATGATGAGAGCTTCAGCTCA	2649
QY	774	TTGATGAGGCTACGCTCCCTGGATTCAAGAACGAACTGAGCTGTCAGGT	833	QY	1854	CAAGAAATTACCTGAGAAGAACGAGATACTGAGCTGAACTGAGCTTGGATTGCGAACAAAGATAG	1913
Db	1570	TTGATGAGGCTACGCTCCCTGGATTCAAGAACGAACTGAGCTGTCAGGT	1629	Db	2650	CAAGAAATTACCTGAGAAGAACGAGATACTGAGCTGAACTGAGCTTGGATTGCGAACAAAGATAG	2709
QY	834	GAGAGGGAGCAAGGTTGGACTACAATGCGTACCCGACTTCGACT	893	QY	1914	TTATATTTTGCCTATGCGAGGGTTCCATTGAGCTTATTCAGCTGGA	1973
Db	1630	GAGAGGGAGCAAGGTTGGACTACAATGCGTACCCGACTTCGACT	1689	Db	2710	TTATATTTTGCCTATGCGAGGGTTCCATTGAGCTTATTCAGCTGGA	2769
QY	894	AGTCGAGATTGATTGACCCCTAACGGATGCTGCGCGAGAACGACAGCT	953	QY	1974	CGATGACCCCCAGGGCATGTCATAGTTTACTGCAATTGCAATTGAGCTATGCC	2033
Db	1690	AGTCGAGATTGATTGACCCCTAACGGATGCTGCGCGAGAACGACAGCT	1749	Db	2770	CGATGACCCCCAGGGCATGTCATAGTTTACTGCAATTGCAATTGAGCTATGCC	2829
QY	954	GAACTAATGCGAAACGGGTCTATATTATCTGATGTCAGGATATAAAA	1013	QY	2034	ATCGAAAAACGCTCGTTGCTCTGATATTCCAAAGCCAAATGGGGCTGCGAT	2093
Db	1750	GAACTAATGCGAAACGGGTCTATATTATCTGATGTCAGGATATAAAA	1013	Db	2830	ATCGAAAAACGCTCGTTGCTCTGATATTCCAAAGCCAAATGGGGCTGCGAT	2889
QY	1014	GCTGATGAGACAGATGAGCTCAATGACATATTCTACTGAGAAGAACCACTACTCT	1073	QY	2094	CTGTTGCCTTGTGGAAAGAACCAATATAGACAGCCGAGTCAGAGGAAAG	2153
Db	1810	GCTGATGAGACAGATGAGCTCAATGACATATTCTACTGAGAAGAACCACTACTCT	1869	Db	2890	CTGTTGCCTTGTGGAAAGAACCAATATAGACAGCCGAGTCAGAGGAAAG	2949
QY	1074	CTGCACTCTGAGAGCATCAAGTCAGACTCATGACAAGGGCTGAGGATCCCAA	1133	QY	2154	CTGACACATGAGGAAATTAGCTTCAGAAGCTCTCTTCATGAGTC	2213
Db	1870	CTGCACTCTGAGAGCATCAAGTCAGACTCATGACAAGGGCTGAGGATCCCAA	1929	Db	2950	CTGACACATGAGGAAATTAGCTTCAGAAGCTCTCTTCATGAGTC	3009
QY	1134	TCTAAAGAGATACTTCTCTGAGGCTCTCTTAAATTAAAGTTAACTAACGCT	1193	QY	2214	CTGAGTTTCATCTCCGCTGCTGAGTTCAGTTCAGTTCAGTTCATGAGTC	2273
Db	1930	TCTAAAGAGATACTTCTCTGAGGCTCTCTTAAATTAAAGTTAACTAACGCT	1989	Db	3010	CTGAGTTTCATCTCCGCTGCTGAGTTCAGTTCAGTTCATGAGTC	3069
QY	1194	GATGCGCTTGTGCTGAGGAACTGGCTCTGCTTAATGAACTGTCATCCA	1253	QY	2274	TTGCGAGGAGGAGGAGCTGCTGAGGAACTTCAGTTCAGTTCAGTTCATGAGACTT	2333
Db	1990	GATGCGCTTGTGCTGAGGAACTGGCTCTGCTTAATGAACTGTCATCCA	2049	Db	3070	TTGCGAGGAGGAGGAGCTGCTGAGGAACTTCAGTTCAGTTCATGAGACTT	3129

Db 1201 AACAGCTCTTCTGAAATTCAAAGCAATTGGGGCTCGCATCTGTTG 1260 ; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-873-409-11

Qy 2101 CTCGTGAAAGAACCAATAATAGACAGCCAGTCAGGAAAGCCAGACA 2160
Db 1261 CTCGTGAAAGAACCAATAATAGACAGCCAGTCAGGAAAGCCAGACA 1320
Qy 2161 CATGTGAAAGGAATTAGATTCGAGAATCTCTTCATTCAGCTGCCAGTG 2220
Db 1321 CATGTGAAAGAACCAATAATAGACAGCCAGTCAGGAAAGCCAGACA 2160
Qy 2221 TTTCATCTCCGCGCTATCCCTCAGTATGAGCGAGAACAGCTAGATTTG 2280
Db 1381 TTTCATCTCCGCGCTATCCCTCAGTATGAGCGAGAACAGCTAGATTTG 1:440
Qy 2281 GAGCACGGCGCTGGAAAGAACACTCTCTGAGCCTAACCAATAATTAC 2340
Db 1441 GAGCACGGCGCTGGAAAGAACACTCTCTGAGCCTAACCAATAATTAC 1500
Qy 2341 TGCAGGACAGTCGCTGTTGATGTTGATGAGAACAGCTGAGAGCTT 2400
Db 1501 TGCAGGACAGTCGCTGTTGATGTTGATGAGAACAGCTGAGAGCTT 1560
Qy 2401 GTTCCAAATAGCAATCGTCCTCAAGAGCCTGCTCTCACTGCGCAATG 2460
Db 1561 GTTCCAAATAGCAATCGTCCTCAAGAGCCTGCTCTCACTGCGCAATG 1620
Qy 2461 ACATGGCTATGGTCAACAGCGCTGTTGCAATTAGATGAGTCAGAAGCC 2520
Db 1621 ACATGGCTATGGTCAACAGCGCTGTTGCAATTAGATGAGTCAGAAGCC 1680
Qy 2521 ATGAGCAATATCCATTCTTATGAGGTCTCCCTGAGAAATACACACAA 2580
Db 1681 ATGAGCAATATCCATTCTTATGAGGTCTCCCTGAGAAATACACACAA 1740
Qy 2581 GACTGAAAGGACACAGCTTCTGGCGSCAGAACAAAGACTAGCTATTG 2640
Db 1741 GACTGAAAGGACACAGCTTCTGGCGSCAGAACAAAGACTAGCTATTG 1800
Qy 2641 TCTCCAAACCAAAATTATGTTGATGAGGCCACTCGCCCTCGATAATG 2700
Db 1801 TCTCCAAACCAAAATTATGTTGATGAGGCCACTCGCCCTCGATAATG 1860
Qy 2701 GTGAGAAGGTGTCAGCTTGTGAGGAAAGGACAGGAGGACATCTCTAG 2760
Db 1861 GTGAGAAGGTGTCAGCTTGTGAGGAAAGGACAGGAGGACATCTCTAG 1920
Qy 2761 TCACTCACAGGCTCTGCAATTCAGAACGCGAAATTGAGGTTCTGCA 2820
Db 1921 TCACTCACAGGCTCTGCAATTCAGAACGCGAAATTGAGGTTCTGCA 1980
Qy 2821 AGATAAAGGACAGGAACATCTCAGAACGCTCTGAGAAATCGAGACAT 2880
Db 1981 AGATAAAGGACAGGAACATCTCAGAACGCTCTGAGAAATCGAGACAT 2040
Qy 2881 TAGTGAATGCACTGAGTGA 2906
Db 2041 TAGTGAATGCACTGAGTGA 2066

RESULT 6
US-09-873-409-11
; Sequence 11, Application US/09873409
; GENERAL INFORMATION:
; APPLICANT: Frank, Markus
; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/288611
; CURRENT APPLICATION NUMBER: US/09/873, 409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; Sequence 16, Application US/09873409
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-873-409-11

Query Match 26.0%; Score 755.2; DB 1; Length 1175;
Best Local Similarity 93.7%; Pred. No. 0.043; Mismatches 3; Indels 50; Gaps 1;
Matches 792; Conservative 0; Mismatches 3; Indels 50; Gaps 1;

Qy 1 CCTAACTCTCTATATCTCTGAGCCTAACCAATAATTATACATCTCT 60
Db 1 CCTAACTCTCTATATCTCTGAGCCTAACCAATAATTATACATCTCT 60
Qy 121 TTAGTGTATCCATAGCTGTTATGCTTGGAGCAGGAGCTCTCA 180
Db 121 TTAGTGTATCCATAGCTGTTATGCTTGGAGCAGGAGCTCTCA 166
Qy 181 CAAATGCGAGGAGCTCTTCAGGTTATGATGAAACCGAGTAG 240
Db 167 -----
Qy 241 ATACTTCCACAGCTGATAAACCTGATCCATAGAACACTGGAATTAA 300
Db 191 ATACTTCCACAGCTGATAAACCTGATCCATAGAACACTGGAATTAA 250
Qy 301 ATGTTCTTCATTATCCATCAAGACCCATCTCAGATTCTGAAGAAGCTCA 360
Db 251 ATGTTCTTCATTATCCATCAAGACCCATCTCAGATTCTGAAGAAGCTCA 310
Qy 361 GAATTAGTCTGAGGAGCAGTGCCTGGTGTCTAACTGCACTGGAGATGG 420
Db 311 GAATTAGTCTGAGGAGCAGTGCCTGGTGTCTAACTGCACTGGAGATGG 370
Qy 421 TAGTCCACTCTGCAAGGTTATGATCCGATGATGGCTTATCATGGGGATGAGA 480
Db 371 TAGTCCACTCTGCAAGGTTATGATCCGATGATGGCTTATCATGGGGATGAGA 430
Qy 481 ATGACATCAGAGCTTAATGTCGGGATATTGAGACCATATGGAGGGTTAGCA 540
Db 431 ATGACATCAGAGCTTAATGTCGGGATATTGAGACCATATGGAGGGTTAGCA 490
Qy 541 ACGCTGTTGTCGGGACACCATCAGTAACATAATCAGATGGAGGAGATGAGA 600
Db 491 ACGCTGTTGTCGGGACACCATCAGTAACATAATCAGATGGAGGAGATGAGA 550
Qy 601 CTGATGAGAGATGGAGGAGCACAGGAGCAATGCPATGATTATCATGAGT 660
Db 551 CTGATGAGAGATGGAGGAGCACAGGAGCAATGCPATGATTATCATGAGT 610
Qy 661 TTCTTAATTAATTAATCATCTGAGGAAAGGCTCAATGAGTGGAGGGAGA 720
Db 611 TTCTTAATTAATTAATCATCTGAGGAAAGGCTCAATGAGTGGAGGGAGA 670
Qy 721 AACAGAGGATCGCAATTGCTCGCCCTAGTCGAAACCCAGATTCGATGAGT 780
Db 671 AACAGAGGATCGCAATTGCTCGCCCTAGTCGAAACCCAGATTCGATGAGT 730
Qy 781 AGCTACTGTCGCCCTGAGATTCAGAACGAACTGTCAGTGGAGAAGG 840
Db 731 AGCTACTGTCGCCCTGAGATTCAGAACGAACTGTCAGTGGAGAAGG 790
Qy 841 CGAC 845
Db 791 ATACC 795

RESULT 7
US-09-873-409-16
; Sequence 16, Application US/09873409

RESULT: B
US-09-873-409-15
Sequence 15, Application US/09873409
GENERAL INFORMATION:
APPLICANT: Frank, Markus
APPLICANT: Sayegh, Mohamed
TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
FILE REFERENCE: 81994/568611
CURRENT APPLICATION NUMBER: US/09/873,409
CURRENT FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 15
LENGTH: 2021
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Note
LOCATION: (23) . (723)
OTHER INFORMATION: n at position 723 represents any nucleotide (A, T, C or G)
US-09-873-409-15

Thu Dec 18 13:40:04 2003

align_ay234788

Page 10

Db	1570	TAGATGAGGTACGTCCTGCCCTGGATTCAAGAAAGCAAGTCAGCTGTTCAAGCTGCACTG	1629
Qy	834	GAGAAGGGAGC	845
Db	1630	GAGNAGGATAC	1641

Search completed: December 18, 2003, 13:02:09
Job time : 34 secs

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: December 18, 2003, 12:57:21 ; Search time 1. Seconds

(without alignments)
4.979 Million cell updates/sec

Title: AAO73470

Perfect score: 4079
Sequence: 1 MVDENDIRALNVRHYRDHG.....gellnrdiYfklvnaqsvq 812

Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 6132 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 8 summaries

Database : US09873409.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	4079	100.0	812	1	US-09-873-409-2	Sequence 2, Appli
2	4079	100.0	1058	1	US-09-873-409-4	Sequence 4, Appli
3	4079	100.0	1195	1	US-09-873-409-5	Sequence 6, Appli
4	4079	100.0	1222	1	US-09-873-409-5	Sequence 5, Appli
5	3323	81.5	659	1	US-09-873-409-1	Sequence 1, Appli
6	828	20.3	514	1	US-09-873-409-8	Sequence 8, Appli
7	812.5	19.9	541	1	US-09-873-409-7	Sequence 7, Appli
8	619	15.2	131	1	US-09-873-409-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-873-409-2
Sequence 2, Application US/09873409

GENERAL INFORMATION:

APPLICANT: Frank, Markus

APPLICANT: Sayegh, Mohamed

TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof

FILE REFERENCE: 81994/268611

CURRENT APPLICATION NUMBER: US/09/873,409

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2
LENGTH: 812

TYPE: PRT

ORGANISM: Homo sapiens

US-09-873-409-2

Query Match

100.0%; Score 4079; DB 1; Length 812;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDENDIRALNVRHYRDHG.....gellnrdiYfklvnaqsvq 812

Db 1 MVDENDIRALNVRHYRDHG.....gellnrdiYfklvnaqsvq 812

QY 121 ALERASKRGTIVIWAHRISTIRSDALIVLTKDGMALAEKGAAHAEIMAKQLYYSILWSDP1 180

Db 121 ALERASKRGTIVIWAHRISTIRSDALIVLTKDGMALAEKGAAHAEIMAKQLYYSILWSDP1 180

QY 181 KKADEQMSMTYSWERKNSLPHYSVKSISDFIKDKEASTQSEKISIPEVSUKILKLN 240

Db 181 KKADEQMSMTYSWERKNSLPHYSVKSISDFIKDKEASTQSEKISIPEVSUKILKLN 240

QY 241 KPEMPFVWGTLASVLN37VHPVSIIFAKITIMFGNDKTLKHDAEYSMFVILGVI 300

Db 241 KPEMPFVWGTLASVLN37VHPVSIIFAKITIMFGNDKTLKHDAEYSMFVILGVI 300

QY 301 CFVSYFMDQSLFYGRAGEITLMRLHLAKFAMLYDIADEKENSTGGLTIAIDIAQ1 360

Db 301 CFVSYFMDQSLFYGRAGEITLMRLHLAKFAMLYDIADEKENSTGGLTIAIDIAQ1 360

QY 361 OGATGCSRIGVLTOMATMGLSVISFPGWMPPLILSAPULAVTGMIETAMTGPARK 420

Db 361 OGATGCSRIGVLTOMATMGLSVISFPGWMPPLILSAPULAVTGMIETAMTGPARK 420

QY 421 DQEIKHAKGKTALENTRITSLTREKAPEQVNEEMLQTOHRNTSKAQIIGSCVAF 480

Db 421 DQEIKHAKGKTALENTRITSLTREKAPEQVNEEMLQTOHRNTSKAQIIGSCVAF 480

QY 481 HAFTYFAYAAGFRFGAYLIQAGRMTPEGMFIIVTAIAGAMAIGKTLVAPETSKAGA 540

Db 481 HAFTYFAYAAGFRFGAYLIQAGRMTPEGMFIIVTAIAGAMAIGKTLVAPETSKAGA 540

QY 541 AHLALLEKCPNTDSRGKPPDCEGMLERFRSPVPCPDPVIFRGLSISERGCT 600

Db 541 AHLALLEKCPNTDSRGKPPDCEGMLERFRSPVPCPDPVIFRGLSISERGCT 600

QY 601 VAFVQSSGCKSTSQVQLQRLYDPVQGQLFDGUDAKELNQMLRSQ1AVPQPVLFN 660

Db 601 VAFVQSSGCKSTSQVQLQRLYDPVQGQLFDGUDAKELNQMLRSQ1AVPQPVLFN 660

QY 661 SIARNTAYGDSNRTVPLDKEAANAAHNSPFLGPEKNTQVGLKAQOLSGGOKORLIA 720

Db 661 SIARNTAYGDSNRTVPLDKEAANAAHNSPFLGPEKNTQVGLKAQOLSGGOKORLIA 720

QY 721 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

Db 721 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

QY 781 LHNGKIKEQGTHQBLRNDIYfklvnaqsvq 812

Db 781 LHNGKIKEQGTHQBLRNDIYfklvnaqsvq 812

QY 843 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

Db 843 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

QY 903 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

Db 903 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

QY 963 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

Db 963 IARALQKPKILLDEASALDNESEKUHQHALDKARTGRTCLVTHRISATIONADLW 780

SEQ ID NO 4
 LENGTH: 1058
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 LOCATION: (66)..(66)
 OTHER INFORMATION: Xaa at position 66 represents any L amino acid
 US-09-873-409-4

Query Match 100.0%; Score 4079; DB 1; Length 1058;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MVEDENDIRALNVRHYDIGHGVSOEPVLFGTISNNIKYGRDVTDEMERAREANAYD 60
 Db 247 MVDENDIRALNVRHYDIGHGVSOEPVLFGTISNNIKYGRDVTDEMERAREANAYD 306

Qy 61 FMEFPNKENTLVGEKGQAMSGQKORIAKARALVRNPKILDEATSALDSBSKAVQA 120
 307 FMEFPNKENTLVGEKGQAMSGQKORIAKARALVRNPKILDEATSALDSBSKAVQA 366

Qy 121 ALEKASKRRTIWAHRSTIRSADLIVTLDKGMLAEGAHAEELMARRGLYSLVMSQDI 180
 367 ALEKASKRRTIWAHRSTIRSADLIVTLDKGMLAEGAHAEELMARRGLYSLVMSQDI 426

Qy 181 KKADEQEMSMYSTERKINSLPLHSVSKISKDFIDKABESTOSKEISLPEVSLKILKLN 240
 427 KKADEQEMSMYSTERKINSLPLHSVSKISKDFIDKABESTOSKEISLPEVSLKILKLN 486

Qy 241 KPEWPFVVLGTLASVLNGTVPFVSIKAITIMFGNDKTLKHDAEYSMIFVILGVI 300
 487 KPEWPFVVLGTLASVLNGTVPFVSIKAITIMFGNDKTLKHDAEYSMIFVILGVI 546

Qy 301 CFVSYFMQGLFGRAGEILTMURHLAKAMLYQDIAMDEKENSTGGLTIAIDIQI 360
 547 CFVSYFMQGLFGRAGEILTMURHLAKAMLYQDIAMDEKENSTGGLTIAIDIQI 606

Qy 361 QATGSRIGVLTQATNGLSVISIPTVGFVWPEVPLIISIAPPVAVTGMETAMGFANK 420
 607 QATGSRIGVLTQATNGLSVISIPTVGFVWPEVPLIISIAPPVAVTGMETAMGFANK 666

Qy 421 DKOELKHAKGKIAATEALENIRTVSLTREKAPEQMYEMLOQHRTSKAQIGSCYAFS 480
 667 DKOELKHAKGKIAATEALENIRTVSLTREKAPEQMYEMLOQHRTSKAQIGSCYAFS 726

Qy 481 HAFIYAYAAGRFRGAYLIQAGRMTPGEMFIVVTAIAGAMAIKTLVAPESKAKSGA 540
 727 HAFIYAYAAGRFRGAYLIQAGRMTPGEMFIVVTAIAGAMAIKTLVAPESKAKSGA 786

Qy 541 AHIFALKEKPNIDSRSOEGKPDTCEGNLFREVSFVPCRDVFLRGLSISIERTKT 600
 787 AHIFALKEKPNIDSRSOEGKPDTCEGNLFREVSFVPCRDVFLRGLSISIERTKT 846

Qy 601 VAvgGSSCGKSTSVOQLRQYDPOGOVLFPGDAKELNOMLRSQIAIVQEPVLFNC 660
 847 VAvgGSSCGKSTSVOQLRQYDPOGOVLFPGDAKELNOMLRSQIAIVQEPVLFNC 906

Qy 661 SIAENIAGDNRSVPLBKEAANANHSFEGLPEKINTQVGLKGAQLSGGQKORLA 720
 907 SIAENIAGDNRSVPLBKEAANANHSFEGLPEKINTQVGLKGAQLSGGQKORLA 966

Qy 721 TARALLOPKILLIDEATSALNDSEKVKQHALDKARTGRTCLVWTHRLSALONADLIVV 780
 967 TARALLOPKILLIDEATSALNDSEKVKQHALDKARTGRTCLVWTHRLSALONADLIVV 1026

Qy 781 LHNQKIKQSGTHOBLRNDIYFKLVNAQSQ 812
 1027 LHNQKIKQSGTHOBLRNDIYFKLVNAQSQ 1058

SEQ ID NO 5
 LENGTH: 1195
 TYPE: PRT
 ORGANISM: Homo sapiens
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 6
 LENGTH: 1195
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-873-409-6

Query Match 100.0%; Score 4079; DB 1; Length 1195;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MVEDENDIRALNVRHYDIGHGVSOEPVLFGTISNNIKYGRDVTDEMERAREANAYD 60
 Db 384 MVEDENDIRALNVRHYDIGHGVSOEPVLFGTISNNIKYGRDVTDEMERAREANAYD 443

Qy 61 FMEFPNKENTLVGEKGQAMSGQKORIAKARALVRNPKILDEATSALDSBSKAVQA 120
 444 FMEFPNKENTLVGEKGQAMSGQKORIAKARALVRNPKILDEATSALDSBSKAVQA 503

Qy 121 ALEKASKRRTIWAHRSTIRSADLIVTLDKGMLAEGAHAEELMARRGLYSLVMSQDI 180
 504 ALEKASKRRTIWAHRSTIRSADLIVTLDKGMLAEGAHAEELMARRGLYSLVMSQDI 563

Qy 181 KKADEQEMSMYSTERKINSLPLHSVSKISKDFIDKABESTOSKEISLPEVSLKILKLN 240
 564 KKADEQEMSMYSTERKINSLPLHSVSKISKDFIDKABESTOSKEISLPEVSLKILKLN 623

Qy 241 KPEWPFVVLGTLASVLNGTVPFVSIKAITIMFGNDKTLKHDAEYSMIFVILGVI 300
 624 KPEWPFVVLGTLASVLNGTVPFVSIKAITIMFGNDKTLKHDAEYSMIFVILGVI 683

Qy 301 CFVSYFMQGLFGRAGEILTMURHLAKAMLYQDIAMDEKENSTGGLTIAIDIQI 360
 684 CFVSYFMQGLFGRAGEILTMURHLAKAMLYQDIAMDEKENSTGGLTIAIDIQI 743

Qy 361 QATGSRIGVLTQATNGLSVISIPTVGFVWPEVPLIISIAPPVAVTGMETAMGFANK 420
 744 QATGSRIGVLTQATNGLSVISIPTVGFVWPEVPLIISIAPPVAVTGMETAMGFANK 803

Qy 421 DKOELKHAKGKIAATEALENIRTVSLTREKAPEQMYEMLOQHRTSKAQIGSCYAFS 480
 804 DKOELKHAKGKIAATEALENIRTVSLTREKAPEQMYEMLOQHRTSKAQIGSCYAFS 863

Qy 481 HAFIYAYAAGRFRGAYLIQAGRMTPGEMFIVVTAIAGAMAIKTLVAPESKAKSGA 540
 864 HAFIYAYAAGRFRGAYLIQAGRMTPGEMFIVVTAIAGAMAIKTLVAPESKAKSGA 923

Qy 541 AHIFALKEKPNIDSRSOEGKPDTCEGNLFREVSFVPCRDVFLRGLSISIERTKT 600
 924 AHIFALKEKPNIDSRSOEGKPDTCEGNLFREVSFVPCRDVFLRGLSISIERTKT 983

Qy 601 VAvgGSSCGKSTSVOQLRQYDPOGOVLFPGDAKELNOMLRSQIAIVQEPVLFNC 660
 984 VAvgGSSCGKSTSVOQLRQYDPOGOVLFPGDAKELNOMLRSQIAIVQEPVLFNC 1043

Qy 661 SIAENIAGDNRSVPLBKEAANANHSFEGLPEKINTQVGLKGAQLSGGQKORLA 720
 961 SIAENIAGDNRSVPLBKEAANANHSFEGLPEKINTQVGLKGAQLSGGQKORLA 1103

Qy 721 TARALLOPKILLIDEATSALNDSEKVKQHALDKARTGRTCLVWTHRLSALONADLIVV 780
 1104 TARALLOPKILLIDEATSALNDSEKVKQHALDKARTGRTCLVWTHRLSALONADLIVV 1163

RESULT 4

Sequence 5, Application US/09873409

GENERAL INFORMATION:

APPLICANT: Frank, Markus

APPLICANT: Sayegh, Mohamed

TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

FILE REFERENCE: 81994/288611

CURRENT APPLICATION NUMBER: US/09/873, 409

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.0

SEQ ID NO 5

LENGTH: 1222

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Note

LOCATION: (210)..(230)

OTHER INFORMATION: Xaa at position 230 represents any L amino acid

US-09-873-409-5

Query Match 100.0%; Score 4079; DB 1; length 1222; Matches 812; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MUDENDRBALNVHYRDHIGWSOEPVLFGTTSNPKYGRDVTDEEMERAARENAVD 60

Db 411 MUENDRDRALNVHYRDHIGWSOEPVLFGTTSNPKYGRDVTDEEMERAARENAVD 470

Qy 61 FIMEPPNPKENTLYGKGAAQMSGGOKQRAIARALWRNPKLILDBATSAALDSSESKAVQA 120

Db 471 FIMEPPNPKENTLYGKGAAQMSGGOKQRAIARALWRNPKLILDBATSAALDSSESKAVQA 530

Qy 121 ALEKASKERTTIVWHLSTIRSADLIVTLKGMLAEKGAAHAEIMAKRGLYSLVMSODI 180

Db 531 ALEKASKERTTIVWHLSTIRSADLIVTLKGMLAEKGAAHAEIMAKRGLYSLVMSODI 590

Qy 181 KKADEQMSMTYSTERKNSPLHSVKSISDFIDKAESTQSKEISLPEVSLIKLKN 240

Db 591 KKADEQMSMTYSTERKNSPLHSVKSISDFIDKAESTQSKEISLPEVSLIKLKN 650

Qy 241 KPEWPFVVLGTLASLWNLGIVHPFESIIFAKITMFGNNDKTTLKDAEISYMSFVVLGVI 300

Db 651 KPEWPFVVLGTLASLWNLGIVHPFESIIFAKITMFGNNDKTTLKDAEISYMSFVVLGVI 710

Qy 301 CFSYPMQGLFYGRAGEILTMRHLAKMFLQDIAWDEKENSTGGTTIADIAQI 360

Db 711 CFSYPMQGLFYGRAGEILTMRHLAKMFLQDIAWDEKENSTGGTTIADIAQI 770

Qy 361 QGATGSRICLVTQNTMGLSVIISPTQWEMPLILSIAPVLAUTGMTEAATGFK 420

Db 771 OGATGSRICLVTQNTMGLSVIISPTQWEMPLILSIAPVLAUTGMTEAATGFK 830

Qy 421 DKOBKHKHACKIATELENTRITVSLTREKAFFEQMEYEMLQTOHNTSKKAQIQGSCYAFS 480

Db 831 DKOBKHKHACKIATELENTRITVSLTREKAFFEQMEYEMLQTOHNTSKKAQIQGSCYAFS 890

Qy 481 HAFYFAYAGFRGAYLIQAGRMPTEGPMPIVFAIAYGAMAGTKVIAPEYSKAKSGA 540

Db 891 HAFYFAYAGFRGAYLIQAGRMPTEGPMPIVFAIAYGAMAGTKVIAPEYSKAKSGA 950

Qy 541 AHLFALLEKKPNIDSRSQCKKPTCEGNEPREVSFFPCRPDWFLRGLSISERKT 600

Db 951 AHLFALLEKKPNIDSRSQCKKPTCEGNEPREVSFFPCRPDWFLRGLSISERKT 1010

Qy 601 VAFVGSSGGCKSTSIVOLLORLYDPWQGQVLFQDGVDAKEIUNQWRSQIAIVPOBPLFNC 660

RESULT 5

Sequence 1, Application US/09873409

GENERAL INFORMATION:

APPLICANT: Frank, Markus

APPLICANT: Sayegh, Mohamed

TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

FILE REFERENCE: 81994/288611

CURRENT APPLICATION NUMBER: US/09/873, 409

CURRENT FILING DATE: 2001-06-05

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 659

TYPE: PRT

ORGANISM: Homo sapiens

US-09-873-409-1

Query Match 81.5%; Score 3323; DB 1; length 659; Matches 659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 154 MLAEGKAAHBLMAKRGGLYSLVMSODIKKADQEMSMTYSTERKNSPLHSVKSISDF 213

Db 1 MLAEGKAAHBLMAKRGGLYSLVMSODIKKADQEMSMTYSTERKNSPLHSVKSISDF 60

Qy 214 IDKAESTQSKEISLPEVSLIKLKNPBEWFLVGLTLASVNGTVPVFSIFAKIT 273

Db 61 IDKAESTQSKEISLPEVSLIKLKNPBEWFLVGLTLASVNGTVPVFSIFAKIT 120

Qy 274 MFGNDKTTLKHDAEISYMSFVVLGVIQCFVSYPMQGLFYGRACRILTMRLRHLAKMFL 333

Db 121 MFGNDKTTLKHDAEISYMSFVVLGVIQCFVSYPMQGLFYGRACRILTMRLRHLAKMFL 180

Qy 334 QIAWDEKENSTGGTTIADIAQIQCATGSRIGVJTONATMGLSVIISITYGMENT 393

Db 181 QIAWDEKENSTGGTTIADIAQIQCATGSRIGVJTONATMGLSVIISITYGMENT 240

Qy 394 FLLISIAPVLAUTGMTEAATGFKQKOEKHAGKATELENTRITVSLTREKAFFQ 453

Db 241 FLLISIAPVLAUTGMTEAATGFKQKOEKHAGKATELENTRITVSLTREKAFFQ 300

Qy 454 MYEEMLQTOHNTSKKAQIQGSCYAFSIIAYGAMAGTKVIAPEYSKAKSGA 513

Db 301 MYEEMLQTOHNTSKKAQIQGSCYAFSIIAYGAMAGTKVIAPEYSKAKSGA 360

Qy 514 TAIAYGAMAGTKVIAPEYSKAKSGA 573

Db 361 TAIAYGAMAGTKVIAPEYSKAKSGA 420

Qy 574 EVSFYFPRPDPFLRGLSISERKT 633

Db 421 EVSFYFPRPDPFLRGLSISERKT 480

Qy 634 VDAKELNQWLSQIAIVPQEPFLNCSIAENAYGDSRVVWDEIKEAANANHSF 653

RESULT 6

US-09-873-409-8

; Sequence 8, Application US/09873409

; GENERAL INFORMATION:

; APPLICANT: Frank, Markus

; APPLICANT: Sayegh, Mohamed

; APPLICANT: Sayegh, Mohamed

; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

; FILE REFERENCE: 81994/268611

; CURRENT APPLICATION NUMBER: US/09/873, 409

; CURRENT FILING DATE: 2001-06-05

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 7

; LENGTH: 541

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: Note

; LOCATION: (230).. (230)

; OTHER INFORMATION: Xaa at position 230 represents any L amino acid

US-09-873-409-7

Query Match 20.3%; Score 828; DB 1; Length 514;

Best Local Similarity 36.7%; Pred. No. 0; Mismatches 103; Indels 202; Gaps 8; Matches 191; Conservative 103; Mismatches 202; Indels 24; Gaps 8;

Query 247 VVGLTASLNGTVHPVSIIFAKILITMGFGNDKTTLKHDAEIS---MIFVILGIVC 301

1 MILGILASLINVAGLPLMPVLGEM---SDNLISGCLVQNTYSFFRLTLVYVGVA 56

Db 302 FVSYFMQGLFYGRAGEILTMRHLAFLKAMLYDIAWDEKENSTGJITIAIDIAQI 361

1 MILGILASLINVAGLPLMPVLGEM---SDNLISGCLVQNTYSFFRLTLVYVGVA 56

Query 57 LIRGYIQISLWITAARQTKRKKQPFHSVLQDIDGFDSCD--IGELNTRMT-DIKIS 113

362 GATGSRIGVLTQNTNGLVSVISFPIWEMTILSTAPVLAUTGMIETAMTGFAKND 421

114 DIGIGDKIAALFQMSFTSIGLAVGLVKWKLTLVTSPLIMASAAACSRMVISJTS 173

Db 362 GATGSRIGVLTQNTNGLVSVISFPIWEMTILSTAPVLAUTGMIETAMTGFAKND 421

114 DIGIGDKIAALFQMSFTSIGLAVGLVKWKLTLVTSPLIMASAAACSRMVISJTS 173

Query 422 KQBLKHAKKIAITALENTITVL-TREKAFEQMY----- 477

422 KQBLKHAKKIAITALENTITVL-TREKAFEQMY----- 477

Db 478 AFSHAFIYFAYAAGPRFGAYLQGR--MTPPEGMPIVTAIAYGAMAIGKTVLVAPEISK 535

234 FPIH-----TGYLAFWYCPSSLILNGEPEYTTGTVLAVFVHSYCYGAAPVHFETAI 289

Query 509 MFIYFTIAYGAMAIGKTVLVAPEISKAGSAHHLALLEKPKNIDSRSORGKPPTEG 568

509 MFIYFTIAYGAMAIGKTVLVAPEISKAGSAHHLALLEKPKNIDSRSORGKPPTEG 568

Db 290 VLAFFFSIHTSSYCYGAAPVHFETATGAFHFTQVIDKPSIONFTSGYKPSIEG 349

569 NLFREPPFVPCRPDVFLGLSLSIERGKTVAFVGSSGKSTSVDQLQRLYDPVQGQ 628

350 TVEFKVNPYSPRSPIKILKGNLRIKSGTETVALVGLNGSKSTVWOLLQRLYDPDDGF 409

Query 629 VLFDGKAKELNQWLRSLQIATVQEPFLFNSIAENIAGDNSRIVPDLDEIKEANAN 688

536 AKGGAHHIFALLEKPKNIDSRSORGKPPTEGKLEPFEVSPYPCRDVFTLRLGSLI 595

290 ARGAFAHFIFOVIDKPKSIDNFTSTGKYPESIESTGVEFKVSTVNPSPRSPIKILKGNLRI 349

596 ERKFTVAFVGSSGKSTSVDQLQRLYDPVQGTVLDFDVKASLNVOMLRSQIAVQEP 655

350 KSGBTVALVGLNGSKSTVWOLLQRLYDPDDGFIVMDENDIRALNVRHYDHTGIVSOPB 409

Query 656 VJFNCIAENIAYCNDNSRIVPDLIKEAANANIHSPFEGLPEKNTQVGLGKAOLSGGQ 715

410 VLFGTISNNIKYGRD--VTDSEEMERAANAYDFTIMEPFPKENTLVGEKGQAMQSGQ 467

Db 716 KORIAIARALLQKKEKILLDEATSLALDNESEKVOHALDK 755

468 KORIAIARALVNPKILILDEATSLALDSESEKSAVQAILEK 507

RESULT 7

US-09-873-409-3

; Sequence 3, Application US/09873409

; GENERAL INFORMATION:

; APPLICANT: Frank, Markus

; APPLICANT: Sayegh, Mohamed

; TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein

; TITLE OF INVENTION: Homologue on Chromosome 7p15-21 and Uses Thereof
; FILE REFERENCE: 81994/268011
; CURRENT APPLICATION NUMBER: US/09/873,409
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-873-409-3

Query Match 15.2%; Score 619; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 1 NVDENDIRALNVRHYRDHIGVVSQEPVLFGTTISNNIKGRDDVDEEMERRARANAYD 60
Db 1 NVDENDIRALNVRHYRDHIGVVSQEPVLFGTTISNNIKGRDDVDEEMERRARANAYD 60
Query 61 FIMEFPNKFNTLVGERGAQMSGGQKRIATARALVRNPKILILDEATSALDSESKAVOA 120
Db 61 FIMEFPNKFNTLVGERGAQMSGGQKRIATARALVRNPKILILDEATSALDSESKAVOA 120
Query 121 ALEK 124
Db 121 ALEK 124

Search completed: December 18, 2003, 12:57:23
Job time : 2 SECS

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